



SEQUENCE LISTING

<110> Kauppinen, Markus Sakari
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<120> Novel Mannanases

<130> 5440.204-US

<140> 09/339,159

<141> 1999-06-24

<150> 60/106,054

<151> 1998-10-28

<150> 60/105,970

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<150> 60/123,543

<151> 1999-03-09

<150> 60/123,623

<151> 1999-03-10

<150> 60/123,641

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<151> 1999-03-11

<160> 34

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<211> 1470

<212> DNA

<213> Bacillus sp. I633

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ggtgacgtcg	atgaagcaac	gattatgagc	tattctgaac	aaagaggagt	tggtggttg	840
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acaactcttt	atgattttga	aggtagtatg	caaggatgga	ctggaagtga	cttgagggga	1080
ggtccttggg	ctgtgacaga	gtggtcttct	aaaggaagtc	attctttaaa	agcggatatt	1140
caattgtcgt	caaattcaca	acattactta	catgttattc	aaaatacgtc	tttacagcag	1200

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JUN 05 2000

TECH CENTER 1600/2500

Ins.
E/21

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ccgattaacg gttcatctgg aacaacgcta tctctagatt tatcaaagt ccaaaatctt 1380
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 <211> 490
 <212> PRT
 <213> Bacillus sp. I633

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Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly
          35          40          45

Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
          50          55          60

Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala Asn
          65          70          75          80

Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp
          85          90          95

Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His Leu
          100          105          110

Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile Ala
          115          120          125

Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala Leu
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Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Phe
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Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala Ile
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Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp Ala
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Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg Glu
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Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His Met
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Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile Asp
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Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
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Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr Ser
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Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly
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Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn Asn
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 305 310 315 320
 Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Gly Gly Gly Ser Asp Gly
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 Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly
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 Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp
 355 360 365
 Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser
 370 375 380
 Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln
 385 390 395 400
 Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val
 405 410 415
 Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr
 420 425 430
 Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr
 435 440 445
 Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg
 450 455 460
 Glu Ile Gly Val Gln Phe Gln Ser Ala Ser Asp Ser Ser Gly Gln Thr
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<211> 1438

<212> DNA

<213> Bacillus sp. I633

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 gaagggattg caaataccgg tgctaatacgt gtccggattg tggtatctga tgggggacaa 180
 tggacaaaag atgacatcca tacagtaaga aaccttatct ctttagcgga agataatcat 240
 ttggttgctg ttctgaagt tcatgatgct accggttatg attccattgc ttcgctcaat 300
 cgtgctgttg attattggat tgaaatgaga agtgctttaa ttggaaagga agataccgtc 360
 attattaata ttgcgaatga atgggttgggt tctgagggaag gggatgcttg ggctgacggg 420
 tataaacaag caatcccgcg attgcgtaac gccgggtctaa accatacctt gatggttagat 480
 gctgcgggggt ggggacaatt tccacaatcg attcatgatt atggaagaga agtttttaat 540
 gctgaccctc aacgaaatac aatgttttgc attcatatgt atgaatatgc aggttggaat 600
 gcatcgcaag ttctactaa tattgaccga gttcttaatc aagacctcgc attagtcatt 660
 ggtgaatttg gacaccgtca taaaaatggt gacgtcgatg aagcaacgat tatgagctat 720
 tctgaacaaa gaggagttgg gtggttggcg tggatcatgga aagggaacgg ccgagaatgg 780
 gagtatttag acctttcgaa tgattgggct ggaaataacc ttacagcttg gggaaatata 840
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acaaataacg cagacaccta ccttgaaata agctttacag gcggaactct tgaaccgggt 1260
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 <213> Bacillus sp.

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 35 40 45
 Asn Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp
 50 55 60
 Asp Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His
 65 70 75 80
 Leu Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile
 85 90 95
 Ala Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala
 100 105 110
 Leu Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp
 115 120 125
 Phe Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala
 130 135 140
 Ile Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp
 145 150 155 160
 Ala Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg
 165 170 175
 Glu Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His
 180 185 190
 Met Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile
 195 200 205
 Asp Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly
 210 215 220
 His Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr
 225 230 235 240
 Ser Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn
 245 250 255
 Gly Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn
 260 265 270
 Asn Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu
 275 280 285
 Arg Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Ala Ser Pro Glu Pro

290		295		300
Thr Pro Glu Pro Thr	Ala Asn Thr Pro Val	Ser Gly Asn Leu Lys Val		
305	310	315	320	
Glu Phe Tyr Asn Ser	Asn Pro Ser Asp Thr Thr	Asn Ser Ile Asn Pro		
	325	330	335	
Gln Phe Lys Val Thr	Asn Thr Gly Ser Ser Ala	Ile Asp Leu Ser Lys		
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Leu Thr Leu Arg Tyr Tyr Tyr	Thr Val Asp Gly Gln Lys Asp	Gln Thr		
	355	360	365	
Phe Trp Cys Asp His Ala Ala	Ile Ile Gly Ser Asn Gly Ser Tyr Asn			
	370	375	380	
Gly Ile Thr Ser Asn Val Lys Gly Thr	Phe Val Lys Met Ser Ser Ser			
	385	390	395	400
Thr Asn Asn Ala Asp Thr Tyr Leu Glu	Ile Ser Phe Thr Gly Gly Thr			
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Leu Glu Pro Gly Ala His Val Gln Ile	Gln Gly Arg Phe Ala Lys Asn			
	420	425	430	
Asp Trp Ser Asn Tyr Thr Gln Ser Asn	Asp Tyr Ser Phe Lys Ser Arg			
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Ser Gln Phe Val Glu Trp Asp Gln Val Thr	Ala Tyr Leu Asn Gly Val			
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 <211> 1482
 <212> DNA
 <213> Bacillus agaradhaerens

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 aatacgttat atgacgcaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
 gcttggtata aagacacgc ttcaacagct attcctgcca ttgcagagca aggcgccaac 240
 acgattcgta ttgttttatc agatggcggt caatgggaaa aagacgacat tgacaccatt 300
 cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcgttga agttcatgat 360
 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420
 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggtat 480
 gggagtggg atggctcagc ttgggccgat ggctatattg atgtcattcc gaagcttcgc 540
 gatgccggct taacacacac cttaattggt gatgcagcag gatgggggca atatccgcaa 600
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 tccatccata tgtatgagta tgctgggtgt gatgctaaca ctggttagatc aaatattgat 720
 agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat 780
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 gaaaatagtc atcatgttag ggaaataggc gtgcaatttt cagcggcaga taatagcagt 1440

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1482

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 <212> PRT
 <213> Bacillus agaradhaerens

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 35 40 45
 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
 50 55 60
 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
 65 70 75 80
 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
 85 90 95
 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
 100 105 110
 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
 115 120 125
 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
 130 135 140
 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
 145 150 155 160
 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
 165 170 175
 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
 180 185 190
 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
 195 200 205
 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
 210 215 220
 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
 225 230 235 240
 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
 245 250 255
 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
 260 265 270
 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
 275 280 285
 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
 290 295 300
 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln

305		310		315		320
Glu Thr Ser Lys	Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His					
	325			330		335
Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr						
	340			345		350
Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr						
	355			360		365
Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu						
	370			375		380
Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu						
	385			390		395
His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly						
	405			410		415
Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser						
	420			425		430
Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn						
	435			440		445
Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His						
	450			455		460
His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser						
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Gly Gln Thr Ala Leu Tyr Val Asp Asn Val Thr Leu Arg						
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 <212> DNA
 <213> Bacillus agaradhaerens

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 aatacggtat atgacgcaaa tgggcagcca ttgtcatga gaggtattaa ccatggacat 180
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 acgattcgta ttgtttttatc agatggcggt caatgggaaa aagacgacat tgacaccatt 300
 cgtgaagtca ttgagcttgc ggagcaaaaat aaaatgggtg ctgtcgttga agttcatgat 360
 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420
 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggtat 480
 gggagttggg atggctcagc ttgggccgat ggctatattg atgtcattcc gaagcttcgc 540
 gatgccggct taacacacac cttaatgggt gatgcagcag gatgggggca atatccgcaa 600
 tctattcatg attacggaca agatgtgttt aatgcagatc cgttaaaaaa tacgatgttc 660
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 <213> Bacillus agaradhaerens

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 35 40 45
 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
 50 55 60
 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
 65 70 75 80
 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
 85 90 95
 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
 100 105 110
 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
 115 120 125
 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
 130 135 140
 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
 145 150 155 160
 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
 165 170 175
 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
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 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
 195 200 205
 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
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 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
 225 230 235 240
 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
 245 250 255
 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
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 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
 275 280 285
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<212> DNA
<213> Bacillus halodurans
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ggttcacagt	caacagggat	gaattcgtact	ggtaacacat	tggattggta	tactcgttta	1020
cttaatgcga	taaaagaaga	tccaaaagca	agtaagattt	cttacattgct	tacatgggca	1080
aactttgggt	tccttaacaa	tatgtattgt	ccctacaag	acattcacgg	tgatttaggt	1140
ggagatcatg	aactccttcc	agatttcatc	aaattttttg	aagatgatta	ctcagctttc	1200
acaggagata	tcaagggaaa	tgtgtatgat	acaggaattg	aatatactgt	agcaccacat	1260
taacggttaa	tgtattgtct	ttcgctatt	actggaacaa	cgtacaacaga	tactgttaca	1320
ttacgagcta	aagtattaaa	cgatgataac	gcagttgtta	cgtaacgggt	tgaaggttct	1380
gacgttgaac	atgaaatgac	gttagctgac	tcgggatact	acacagctaa	gtattctccg	1440
acggcagaag	taaattggtgg	atcagttgat	ttaacagtta	cgtactgggtc	tggagaagaa	1500
aaagtacaag	atgaagtgat	tagactttat	gtaaaggctt	cagaaatctc	actttacaag	1560
cttacgtttg	atgaggat	taatggaatt	aagtcgaatg	gcacttggcc	tgaagatggt	1620
attacatctg	acgtttctca	tgctagtttt	gacggaaatg	ggaaattgaa	gatttcagtt	1680
aatggaatgt	catccgaaga	gtggtggcaa	gaacttaaat	tagaattaac	gqatctttct	1740

gatgtgaatt tagccaagta a

1761

<210> 10
 <211> 586
 <212> PRT
 <213> Bacillus halodurans

<400> 10
 Met Lys Ser Ile Lys Lys Leu Val Val Val Cys Met Ala Phe Leu Leu
 1 5 10 15
 Ile Phe Pro Ser Thr Ser Phe Ala Phe Ser Gly Ser Val Ser Ala Ser
 20 25 30
 Gly Gln Glu Leu Lys Met Thr Asp Gln Asn Ala Ser Gln Tyr Thr Lys
 35 40 45
 Glu Leu Phe Ala Phe Leu Arg Asp Val Ser Gly Lys Gln Val Leu Phe
 50 55 60
 Gly Gln Gln His Ala Thr Asp Glu Gly Leu Thr Leu Arg Gly Thr Gly
 65 70 75 80
 Asn Arg Ile Gly Ser Thr Glu Ser Glu Val Lys Asn Ala Val Gly Asp
 85 90 95
 Tyr Pro Ala Val Phe Gly Trp Asp Thr Asn Ser Leu Asp Gly Arg Glu
 100 105 110
 Lys Pro Gly Asn Asp Glu Pro Ser Gln Glu Gln Arg Ile Leu Asn Thr
 115 120 125
 Ala Ala Ser Met Lys Ala Ala His Asp Leu Gly Gly Ile Ile Thr Leu
 130 135 140
 Ser Met His Pro Asp Asn Phe Val Thr Gly Gly Ala Tyr Gly Asp Thr
 145 150 155 160
 Thr Gly Asn Val Val Gln Glu Ile Leu Pro Gly Gly Ser Lys His Glu
 165 170 175
 Glu Phe Asn Ala Trp Leu Asp Asn Leu Ala Ala Leu Ala His Glu Leu
 180 185 190
 Lys Asp Asp Asn Gly Lys His Ile Pro Ile Ile Phe Arg Pro Phe His
 195 200 205
 Glu Gln Thr Gly Ser Trp Phe Trp Trp Gly Ala Ser Thr Thr Thr Pro
 210 215 220
 Glu Gln Tyr Lys Ala Ile Tyr Arg Tyr Thr Val Glu Tyr Leu Arg Asp
 225 230 235 240
 Val Lys Gly Ala Asn Asn Phe Leu Tyr Gly Phe Ser Pro Gly Ala Gly
 245 250 255
 Pro Ala Gly Asp Leu Asn Arg Tyr Met Glu Thr Tyr Pro Gly Asp Asp
 260 265 270
 Tyr Val Asp Ile Phe Gly Ile Asp Asn Tyr Asp Asn Lys Ser Asn Ala
 275 280 285
 Gly Ser Glu Ala Trp Ile Gln Gly Val Val Thr Asp Leu Ala Met Leu
 290 295 300

Val Asp Leu Ala Glu Glu Lys Gly Lys Ile Ala Ala Phe Thr Glu Tyr
 305 310 315 320
 Gly Tyr Ser Ala Thr Gly Met Asn Arg Thr Gly Asn Thr Leu Asp Trp
 325 330 335
 Tyr Thr Arg Leu Leu Asn Ala Ile Lys Glu Asp Pro Lys Ala Ser Lys
 340 345 350
 Ile Ser Tyr Met Leu Thr Trp Ala Asn Phe Gly Phe Pro Asn Asn Met
 355 360 365
 Tyr Val Pro Tyr Lys Asp Ile His Gly Asp Leu Gly Gly Asp His Glu
 370 375 380
 Leu Leu Pro Asp Phe Ile Lys Phe Phe Glu Asp Asp Tyr Ser Ala Phe
 385 390 395 400
 Thr Gly Asp Ile Lys Gly Asn Val Tyr Asp Thr Gly Ile Glu Tyr Thr
 405 410 415
 Val Ala Pro His Glu Arg Leu Met Tyr Val Leu Ser Pro Ile Thr Gly
 420 425 430
 Thr Thr Ile Thr Asp Thr Val Thr Leu Arg Ala Lys Val Leu Asn Asp
 435 440 445
 Asp Asn Ala Val Val Thr Tyr Arg Val Glu Gly Ser Asp Val Glu His
 450 455 460
 Glu Met Thr Leu Ala Asp Ser Gly Tyr Tyr Thr Ala Lys Tyr Ser Pro
 465 470 475 480
 Thr Ala Glu Val Asn Gly Gly Ser Val Asp Leu Thr Val Thr Tyr Trp
 485 490 495
 Ser Gly Glu Glu Lys Val Gln Asp Glu Val Ile Arg Leu Tyr Val Lys
 500 505 510
 Ala Ser Glu Ile Ser Leu Tyr Lys Leu Thr Phe Asp Glu Asp Ile Asn
 515 520 525
 Gly Ile Lys Ser Asn Gly Thr Trp Pro Glu Asp Gly Ile Thr Ser Asp
 530 535 540
 Val Ser His Val Ser Phe Asp Gly Asn Gly Lys Leu Lys Phe Ala Val
 545 550 555 560
 Asn Gly Met Ser Ser Glu Glu Trp Trp Gln Glu Leu Lys Leu Glu Leu
 565 570 575
 Thr Asp Leu Ser Asp Val Asn Leu Ala Lys
 580 585

<210> 11
 <211> 995
 <212> DNA
 <213> Bacillus sp. AAI12

<400> 11
 gtgtataagc ttacccatac gtatatttgggt gogttaattt gttctatttt gatctttgct 60
 ggggttttaa atacttcttc ttcacaagca gaagcccatc acagtgggtt ccatgttaat 120
 ggtacaacat tatatgatgc aaatggaaac ccttttggtta tgagagggat taatcatgga 180
 catgcttggt ttaaacaaga actagaaaca tccatgagag ggattagtca aacaggggca 240
 aatacgattc gtgtcgtttt gtctaattggg caaagatggc aaaaagatga tcgaaacatg 300

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gtagcttcgg ttatttcttt ggcagagcag catcaaataa ttgccgtttt agaagttcat 360
gatgctactg gtagcaataa tttctccgat ctgcaagctg ctgtggacta ttggattgag 420
atgaaggatg ttttgcaggg gaaagaggac atagtgatca ttaatatcgc caatgaatgg 480
tacgggtgctt gggacggagg cgcattgggca cgaggggtatc agaatgcat acgtcagctt 540
cgaaatgcag gcttgtcaca tacatttatg gttgacgctg ccggttatgg ccagtacct 600
caatcggtag ttgattatgg tcaagaagta ttaaagtctg acccacagag aaacacaatg 660
ttttctgttc atatgtatga atatgcaggc ggagatgcta atacagtaag acgaaacatt 720
gactcgatct taagccagaa cttagctctt gtcattgggtg aattcgggca ttggcattat 780
gacgggtgatg ttgatgagga caccatttta agctattcac agcaaagaaa tgtgggatgg 840
ttggcgtagga gctggcatgg caatagtga ggggtcgaat atcttgattt atcgaatgac 900
tttgctggta atcgactgac atgggtgggt gatcgaatag taaacggtcc gaatgggatt 960
cgtcaaacct ctaaaagaag cagtgtgttt caata 995

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<210> 12
 <211> 331
 <212> PRT
 <213> Bacillus sp. AAI12

<400> 12
 Val Tyr Lys Leu Thr His Thr Tyr Phe Val Ala Leu Ile Cys Ser Ile
 1 5 10 15
 Leu Ile Phe Ala Gly Val Leu Asn Thr Ser Ser Ser Gln Ala Glu Ala
 20 25 30
 His His Ser Gly Phe His Val Asn Gly Thr Thr Leu Tyr Asp Ala Asn
 35 40 45
 Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Phe
 50 55 60
 Lys Gln Glu Leu Glu Thr Ser Met Arg Gly Ile Ser Gln Thr Gly Ala
 65 70 75 80
 Asn Thr Ile Arg Val Val Leu Ser Asn Gly Gln Arg Trp Gln Lys Asp
 85 90 95
 Asp Arg Asn Met Val Ala Ser Val Ile Ser Leu Ala Glu Gln His Gln
 100 105 110
 Met Ile Ala Val Leu Glu Val His Asp Ala Thr Gly Ser Asn Asn Phe
 115 120 125
 Ser Asp Leu Gln Ala Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Val
 130 135 140
 Leu Gln Gly Lys Glu Asp Ile Val Ile Ile Asn Ile Ala Asn Glu Trp
 145 150 155 160
 Tyr Gly Ala Trp Asp Gly Gly Ala Trp Ala Arg Gly Tyr Gln Asn Ala
 165 170 175
 Ile Arg Gln Leu Arg Asn Ala Gly Leu Ser His Thr Phe Met Val Asp
 180 185 190
 Ala Ala Gly Tyr Gly Gln Tyr Pro Gln Ser Val Val Asp Tyr Gly Gln
 195 200 205
 Glu Val Leu Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Val His
 210 215 220
 Met Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Arg Asn Ile
 225 230 235 240
 Asp Ser Ile Leu Ser Gln Asn Leu Ala Leu Val Ile Gly Glu Phe Gly
 245 250 255

His Trp His Tyr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr
 260 265 270

Ser Gln Gln Arg Asn Val Gly Trp Leu Ala Trp Ser Trp His Gly Asn
 275 280 285

Ser Glu Gly Val Glu Tyr Leu Asp Leu Ser Asn Asp Phe Ala Gly Asn
 290 295 300

Arg Leu Thr Trp Trp Gly Asp Arg Ile Val Asn Gly Pro Asn Gly Ile
 305 310 315 320

Arg Gln Thr Ser Lys Arg Ser Ser Val Phe Gln
 325 330

<210> 13
 <211> 1464
 <212> DNA
 <213> Humicola insolens

<400> 13
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 gccgctcctt actgtgctcc ccagccgctc acaacctctc aggagcctac gagcactccg 120
 tcgcctgtgc ccggtcccg gaccttcgaa gccggaggatg ccatcctcac gggcacgagg 180
 gttgagtcga gcctcgccgg ctactctggt accggatatg tagcgggctt cgacgagccc 240
 agtgacaaga tcacgttcca cgtggacagc gagaccacac ggctgtacga cctcaccatc 300
 cgcgtagccg ccatctatgg cgagaagcgc accaccgctc tgctcaataa cggcgcgcca 360
 agtgaggtct acttcccggc aggcgattcg ttcgtcgaca tcgctgccgg ccaggtcctg 420
 ctgaaccagg gcgacaacac catcgacatt gtcaacaact ggggatggta cctgatcgac 480
 tccatcacca tcacccctc cgcgccgga cccctcacc aaatcaacc ttccccgctc 540
 aaccctgccg ccgacgacaa cgcgcgggcg ttgtacgcat acctccgctc catctacggc 600
 aagaaaatcc tttccggcca gcaggagctt tcctgggcga actggatcgc ccaacagacg 660
 ggcaaaaactc ccgcgctggg gtccgtcgat atgatggatt attcccctag tcgggtggaa 720
 agaggcactg tcgggtctgc cgtcgaggag gccatcgagc atcaccggcg cggcggcatt 780
 gtctcgggtg tgtggcactg gaacgcgcc acggggctgt acgacacgcc cgagcgccgg 840
 tggtaggagc ggttctacac ggacgcgacc gactttgacg tcgcgcgggc gctggcgat 900
 acgacgaatg ccaactacac gctgctgac cgggatatcg acgcatcgc ggtgcagctc 960
 aagaggttgc gggacgcggg cgtgccgggt ctttggcgcc cgctgcacga ggccgagggc 1020
 ggttggtttt ggtggggagc gaagggccc gaggcatata agaagctgtg ggggattctg 1080
 tatgaccgac tcacgaacta ccatgggctg aataacctgc tgtgggtgtg gaactcgatc 1140
 ctacccgagt ggtatcccgg agacgaaaca gtagacattg tcagcgcgga cgtgtacgag 1200
 cagggtaatg ggcccatgtc gacgcagtat aaccagctca tcgagctggg caaggacaag 1260
 aagatgatcg cggcgactga ggtcggggcc gcgccgctgc cggacctgtt gcaggcctat 1320
 gaggtcact ggttgtggtt cgctgtttgg ggagacacgt tcatcaacaa ccctcagtgg 1380
 aactcgatcg agaccttgaa gacgatctac aatagcgact atgttctcac tctcgatgag 1440
 attcaggggt ggaggaacgc gcaa 1464

<210> 14
 <211> 488
 <212> PRT
 <213> Humicola insolens

<400> 14
 Met Ala Lys Ala Leu Lys Tyr Phe Ala Trp Gly Leu Ala Ala Leu Ala
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Ser Gly Ala Val Ala Ala Pro Tyr Cys Ala Pro Gln Pro Ser Thr Thr
 20 25 30

Ser Gln Glu Pro Thr Ser Thr Pro Ser Pro Val Pro Gly Pro Arg Thr
 35 40 45

Phe Glu Ala Glu Asp Ala Ile Leu Thr Gly Thr Arg Val Glu Ser Ser
 50 55 60

Leu Ala Gly Tyr Ser Gly Thr Gly Tyr Val Ala Gly Phe Asp Glu Pro
 65 70 75 80
 Ser Asp Lys Ile Thr Phe His Val Asp Ser Glu Thr Thr Arg Leu Tyr
 85 90 95
 Asp Leu Thr Ile Arg Val Ala Ala Ile Tyr Gly Glu Lys Arg Thr Thr
 100 105 110
 Val Val Leu Asn Asn Gly Ala Ala Ser Glu Val Tyr Phe Pro Ala Gly
 115 120 125
 Asp Ser Phe Val Asp Ile Ala Ala Gly Gln Val Leu Leu Asn Gln Gly
 130 135 140
 Asp Asn Thr Ile Asp Ile Val Asn Asn Trp Gly Trp Tyr Leu Ile Asp
 145 150 155 160
 Ser Ile Thr Ile Thr Pro Ser Ala Pro Arg Pro Pro His Gln Ile Asn
 165 170 175
 Pro Ser Pro Val Asn Pro Ala Ala Asp Asp Asn Ala Arg Ala Leu Tyr
 180 185 190
 Ala Tyr Leu Arg Ser Ile Tyr Gly Lys Lys Ile Leu Ser Gly Gln Gln
 195 200 205
 Glu Leu Ser Trp Ala Asn Trp Ile Ala Gln Gln Thr Gly Lys Thr Pro
 210 215 220
 Ala Leu Val Ser Val Asp Met Met Asp Tyr Ser Pro Ser Arg Val Glu
 225 230 235 240
 Arg Gly Thr Val Gly Ser Ala Val Glu Glu Ala Ile Glu His His Arg
 245 250 255
 Arg Gly Gly Ile Val Ser Val Leu Trp His Trp Asn Ala Pro Thr Gly
 260 265 270
 Leu Tyr Asp Thr Pro Glu Arg Arg Trp Trp Ser Gly Phe Tyr Thr Asp
 275 280 285
 Ala Thr Asp Phe Asp Val Ala Arg Ala Leu Ala Asp Thr Thr Asn Ala
 290 295 300
 Asn Tyr Thr Leu Leu Ile Arg Asp Ile Asp Ala Ile Ala Val Gln Leu
 305 310 315 320
 Lys Arg Leu Arg Asp Ala Gly Val Pro Val Leu Trp Arg Pro Leu His
 325 330 335
 Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ala
 340 345 350
 Tyr Lys Lys Leu Trp Gly Ile Leu Tyr Asp Arg Leu Thr Asn Tyr His
 355 360 365
 Gly Leu Asn Asn Leu Leu Trp Val Trp Asn Ser Ile Leu Pro Glu Trp
 370 375 380
 Tyr Pro Gly Asp Glu Thr Val Asp Ile Val Ser Ala Asp Val Tyr Ala
 385 390 395 400
 Gln Gly Asn Gly Pro Met Ser Thr Gln Tyr Asn Gln Leu Ile Glu Leu
 405 410 415

Gly Lys Asp Lys Lys Met Ile Ala Ala Thr Glu Val Gly Ala Ala Pro
 420 425 430
 Leu Pro Asp Leu Leu Gln Ala Tyr Glu Ala His Trp Leu Trp Phe Ala
 435 440 445
 Val Trp Gly Asp Thr Phe Ile Asn Asn Pro Gln Trp Asn Ser Ile Glu
 450 455 460
 Thr Leu Lys Thr Ile Tyr Asn Ser Asp Tyr Val Leu Thr Leu Asp Glu
 465 470 475 480
 Ile Gln Gly Trp Arg Asn Ala Gln
 485

<210> 15
 <211> 1107
 <212> DNA
 <213> Bacillus sp. AA349

<400> 15
 atgagaagta tgaagctttt atttgctatg tttattttag ttttttcttc ttttaactttt 60
 aacttagtag ttgcgcaagc tagtggacat gggcaaagtc ataaagtacc ttggggcacca 120
 caagctgaag caccctggaaa aacggctgaa aatggagctc gggataaagt tcgaaataat 180
 cctggaaaag ccaatcctcc agcaggaaaa gtcaatgggt tttatataga tggaacaacc 240
 ttatatgatg caaatggtaa gccatttggt atgcgtggaa ttaaccacgg tcattcatgg 300
 tacaagcctc acatagaaac cgcgatggag gcaattgctg atactggagc aaactccatt 360
 cgtgtagttc tctcagatgg acaacagtg accaaagatg atgttgacga agtagcaaaa 420
 attatatctt tagcagaaaa acattcttta gttgctgctc ttgaggtaca tgatgcactc 480
 ggaacagatg atattgaacc attacttaaa acagttgatt actggattga gatcaaagat 540
 gctttaatcg gaaaagagga caaagtaatt attaacattt ctaatgaatg gtttggttct 600
 tggagcagtg aaggttgggc agatggatat aaaaaagcaa ttcctttact aagagaggcg 660
 ggtctaaaac atacacttat ggttgacgca gctgggtggg gacaatttcc tagatctatt 720
 catgaaaaag gattagaagt ttttaactca gacccattaa agaatacaat gttttccatt 780
 catatgtatg aatgggcagc gggtaatcct caacaagtaa aagacaatat tgacgggtgt 840
 cttgaaaaga atttagctgt agtaattggt gagttcggtc atcatcacta cggaagagat 900
 gttgctgttg atacaatctt aagtcattct gagaagtatg atgtaggttg gcttgcttgg 960
 tcttggcacg gaaatagtgg tgggtgtagag tatcttgact tagcaacaga tttctcaggg 1020
 acacaactaa ctgaatgggg agaaagaatt gtacacggtc cgaatgggtt aaaagaaact 1080
 tctgaaatcg ttagtgtata caaaaaa 1107

<210> 16
 <211> 369
 <212> PRT
 <213> Bacillus sp. AA349

<400> 16
 Met Arg Ser Met Lys Leu Leu Phe Ala Met Phe Ile Leu Val Phe Ser
 1 5 10 15
 Ser Phe Thr Phe Asn Leu Val Val Ala Gln Ala Ser Gly His Gly Gln
 20 25 30
 Met His Lys Val Pro Trp Ala Pro Gln Ala Glu Ala Pro Gly Lys Thr
 35 40 45
 Ala Glu Asn Gly Val Trp Asp Lys Val Arg Asn Asn Pro Gly Lys Ala
 50 55 60
 Asn Pro Pro Ala Gly Lys Val Asn Gly Phe Tyr Ile Asp Gly Thr Thr
 65 70 75 80
 Leu Tyr Asp Ala Asn Gly Lys Pro Phe Val Met Arg Gly Ile Asn His
 85 90 95

Gly His Ser Trp Tyr Lys Pro His Ile Glu Thr Ala Met Glu Ala Ile
 100 105 110
 Ala Asp Thr Gly Ala Asn Ser Ile Arg Val Val Leu Ser Asp Gly Gln
 115 120 125
 Gln Trp Thr Lys Asp Asp Val Asp Glu Val Ala Lys Ile Ile Ser Leu
 130 135 140
 Ala Glu Lys His Ser Leu Val Ala Ala Leu Glu Val His Asp Ala Leu
 145 150 155 160
 Gly Thr Asp Asp Ile Glu Pro Leu Leu Lys Thr Val Asp Tyr Trp Ile
 165 170 175
 Glu Ile Lys Asp Ala Leu Ile Gly Lys Glu Asp Lys Val Ile Ile Asn
 180 185 190
 Ile Ser Asn Glu Trp Phe Gly Ser Trp Ser Ser Glu Gly Trp Ala Asp
 195 200 205
 Gly Tyr Lys Lys Ala Ile Pro Leu Leu Arg Glu Ala Gly Leu Lys His
 210 215 220
 Thr Leu Met Val Asp Ala Ala Gly Trp Gly Gln Phe Pro Arg Ser Ile
 225 230 235 240
 His Glu Lys Gly Leu Glu Val Phe Asn Ser Asp Pro Leu Lys Asn Thr
 245 250 255
 Met Phe Ser Ile His Met Tyr Glu Trp Ala Ala Gly Asn Pro Gln Gln
 260 265 270
 Val Lys Asp Asn Ile Asp Gly Val Leu Glu Lys Asn Leu Ala Val Val
 275 280 285
 Ile Gly Glu Phe Gly His His His Tyr Gly Arg Asp Val Ala Val Asp
 290 295 300
 Thr Ile Leu Ser His Ser Glu Lys Tyr Asp Val Gly Trp Leu Ala Trp
 305 310 315 320
 Ser Trp His Gly Asn Ser Gly Gly Val Glu Tyr Leu Asp Leu Ala Thr
 325 330 335
 Asp Phe Ser Gly Thr Gln Leu Thr Glu Trp Gly Glu Arg Ile Val His
 340 345 350
 Gly Pro Asn Gly Leu Lys Glu Thr Ser Glu Ile Val Ser Val Tyr Lys
 355 360 365

Lys

<210> 17
 <211> 915
 <212> DNA
 <213> Bacillus sp.

<400> 17
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 ggacaaaatt catcgccaat taaagcttat ggcaacgaag tgtaaacca tgatccgcag 120
 cgcaatgtta tgttctccat acacatgtac ggttcctgga ataatcagtc gcgaatcggc 180
 agcgaattgc aggccatcaa agaccttggg cttgctgtca tgattggtga attcggatac 240
 aactacaaca acggcaataa caacttgggg agtcagggtta acgcccagga aatcatgaat 300


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caggcgcaag caaaaggaat cggctacatg ccggtggtcgt ggactggcaa tgacgcggct 360
aactcttggg tggatatgac aacaaacgat tggcaaacac ttacatcatg ggggaatcta 420
gttgtaaata gaaccaacgg cattcgagct acgtctgtcc cagcaactgt atttaataca 480
caaacaacaa tttatgattt tgaaggcggc aatgcccagg gctggtcagg ttccggtttg 540
agcggggggg cttggtctgt taatgaatgg gcggcgagcg gtagttattc tctcaaagcg 600
aatatatctc taggcgccac tcaaaaagct ttgcaaacca cagcgtccca taatttcagc 660
ggccggtcta cattatccgt aagagtaaag catgcagcat ggggaaatca cggcagcggg 720
atgcaagcca agttatatgt gaaaacaggg gccggttacg cctggtatga tggcggcact 780
gtaaacatca acagctcggg caacacattg acgctaaacc tggcaggcat tcctaattctg 840
aacgacgtca gagaactcgg aattgaattt ataacacctg caaattcgag tggttctttc 900
gcaatttatg ttgac 915

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<210> 18
 <211> 305
 <212> PRT
 <213> Bacillus sp.

<400> 18
 Ile Ser Thr Leu Arg Asn Ala Gly Ile Arg Asn Thr Ile Val Val Asp
 1 5 10 15
 Ala Ser Gly Trp Gly Gln Asn Ser Ser Pro Ile Lys Ala Tyr Gly Asn
 20 25 30
 Glu Val Leu Asn His Asp Pro Gln Arg Asn Val Met Phe Ser Ile His
 35 40 45
 Met Tyr Gly Ser Trp Asn Asn Gln Ser Arg Ile Gly Ser Glu Leu Gln
 50 55 60
 Ala Ile Lys Asp Leu Gly Leu Ala Val Met Ile Gly Glu Phe Gly Tyr
 65 70 75 80
 Asn Tyr Asn Asn Gly Asn Asn Asn Leu Gly Ser Gln Val Asn Ala Gln
 85 90 95
 Glu Ile Met Asn Gln Ala Gln Ala Lys Gly Ile Gly Tyr Met Pro Trp
 100 105 110
 Ser Trp Thr Gly Asn Asp Ala Ala Asn Ser Trp Leu Asp Met Thr Thr
 115 120 125
 Asn Asp Trp Gln Thr Leu Thr Ser Trp Gly Asn Leu Val Val Asn Gly
 130 135 140
 Thr Asn Gly Ile Arg Ala Thr Ser Val Pro Ala Thr Val Phe Asn Thr
 145 150 155 160
 Gln Thr Thr Ile Tyr Asp Phe Glu Gly Gly Asn Ala Gln Gly Trp Ser
 165 170 175
 Gly Ser Gly Leu Ser Gly Gly Pro Trp Ser Val Asn Glu Trp Ala Ala
 180 185 190
 Ser Gly Ser Tyr Ser Leu Lys Ala Asn Ile Ser Leu Gly Ala Thr Gln
 195 200 205
 Lys Ala Leu Gln Thr Thr Ala Ser His Asn Phe Ser Gly Arg Ser Thr
 210 215 220
 Leu Ser Val Arg Val Lys His Ala Ala Trp Gly Asn His Gly Ser Gly
 225 230 235 240
 Met Gln Ala Lys Leu Tyr Val Lys Thr Gly Ala Gly Tyr Ala Trp Tyr
 245 250 255

Asp Gly Gly Thr Val Asn Ile Asn Ser Ser Gly Asn Thr Leu Thr Leu
 260 265 270

Asn Leu Ala Gly Ile Pro Asn Leu Asn Asp Val Arg Glu Leu Gly Ile
 275 280 285

Glu Phe Ile Thr Pro Ala Asn Ser Ser Gly Ser Phe Ala Ile Tyr Val
 290 295 300

Asp
 305

<210> 19
 <211> 397
 <212> DNA
 <213> *Bacillus clausii*

<400> 19
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 ggattggcgc aaactggatt tcaagtaaca gggacccagt tgcttgatgg agagggcaat 120
 ccgtatgtga tgcgtggagt caatcacgga cattcatggt tcaaacaaga ccttgataca 180
 gcaataccag ctattgcagc gactggcgct aatacggtga gaatcgtttt atcgaatggc 240
 caacaatggg agcgagatac cgtagcggaa gttgaaagag tgcttgcagt taccgaagag 300
 gaaggcttga cggctgtact tgaagttcat gatgcgacgg gaagtgatga tccaaacgat 360
 ttgtttactg cagtggagta ttggtcagag agaggat 397

<210> 20
 <211> 132
 <212> PRT
 <213> *Bacillus clausii*

<400> 20
 Ile Ser Gln Gly Leu Val Gly Val Ile Ile Leu Leu Tyr Met Ala Phe
 1 5 10 15

Ser Gln Glu Arg Gly Leu Ala Gln Thr Gly Phe Gln Val Thr Gly Thr
 20 25 30

Gln Leu Leu Asp Gly Glu Gly Asn Pro Tyr Val Met Arg Gly Val Asn
 35 40 45

His Gly His Ser Trp Phe Lys Gln Asp Leu Asp Thr Ala Ile Pro Ala
 50 55 60

Ile Ala Ala Thr Gly Ala Asn Thr Val Arg Ile Val Leu Ser Asn Gly
 65 70 75 80

Gln Gln Trp Glu Arg Asp Thr Val Ala Glu Val Glu Arg Val Leu Ala
 85 90 95

Val Thr Glu Glu Glu Gly Leu Thr Ala Val Leu Glu Val His Asp Ala
 100 105 110

Thr Gly Ser Asp Asp Pro Asn Asp Leu Phe Thr Ala Val Glu Tyr Trp
 115 120 125

Ser Glu Arg Gly
 130

<210> 21
 <211> 960
 <212> DNA
 <213> Bacillus sp.

<400> 21
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 tacagtagcg gtttagcatc tgcacaaagc ggctttcacg taaaagggtac agagttgttg 120
 gacaaaaatg gcgatcctta cgttatgcgt ggcgtaacc atggacattc ttggttttaa 180
 caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240
 gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300
 gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360
 gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420
 aaggggacag aagaccgggt aatcattaac attgccaatg aatggtatgg ggctgggagg 480
 agtgacgttt gggcagaggc atacgcacaa gcgatccgcg ccttgccgag tgctggcctc 540
 gcccatacgt taatagttga tgcggcaggt tggggacagt accctgcctc tatccatgag 600
 cggggagccg acgtatttgc ctccgatcca ttaaaaaaca caatgttttc catccatag 660
 tacgaatatg caggacgga tagggcgaca gtttctgaaa acatcgacgg tgtacttgct 720
 gaaaatcctt ctgtggtaat cgggtgaattt ggccataggc atcatgatgg cgtatgcat 780
 gaagatgcga ttttggccta tacagcagag cggcaagtgg gctggccttg ctggtcatgg 840
 tatggcaata gcgggggtgt tgaatacttg gatttaactg aaggcccatc aggtccatta 900
 acgagttggg gcgaacggat tgtctatggg gaaatgggct taaaagtaat tgatcacttg 960

<210> 22
 <211> 320
 <212> PRT
 <213> Bacillus sp.

<400> 22
 Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Val Val Leu
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 Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe
 20 25 30
 His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val
 35 40 45
 Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu
 50 55 60
 Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile
 65 70 75 80
 Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu
 85 90 95
 Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu
 100 105 110
 Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys
 115 120 125
 Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu
 130 135 140
 Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg
 145 150 155 160
 Ser Asp Val Trp Ala Glu Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg
 165 170 175
 Ser Ala Gly Leu Ala His Thr Leu Ile Val Asp Ala Ala Gly Trp Gly
 180 185 190

Gln Tyr Pro Ala Ser Ile His Glu Arg Gly Ala Asp Val Phe Ala Ser
 195 200 205

Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met Tyr Glu Tyr Ala
 210 215 220

Gly Ala Asp Arg Ala Thr Val Ser Glu Asn Ile Asp Gly Val Leu Ala
 225 230 235 240

Glu Asn Leu Ala Val Val Ile Gly Glu Phe Gly His Arg His His Asp
 245 250 255

Gly Asp Val Asp Glu Asp Ala Ile Leu Ala Tyr Thr Ala Glu Arg Gln
 260 265 270

Val Gly Trp Leu Ala Trp Ser Trp Tyr Gly Asn Ser Gly Gly Val Glu
 275 280 285

Tyr Leu Asp Leu Thr Glu Gly Pro Ser Gly Pro Leu Thr Ser Trp Gly
 290 295 300

Glu Arg Ile Val Tyr Gly Glu Met Gly Leu Lys Val Ile Asp His Leu
 305 310 315 320

<210> 23
 <211> 564
 <212> DNA
 <213> Bacillus sp.

<400> 23
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 gacaaaaatg gcgatcctta cgttatgcgt ggcgtcaacc atggacattc ttggtttaaa 180
 caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240
 gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300
 gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360
 gataatcccc atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420
 aaggggacag aagaccgggt aatcattaac attgccaatg aatggtatgg ggcgtggagg 480
 agtgaccctt gggcaaaagc atacgcacaa gcgatcccgc gcttgccgag tgctggcctc 540
 gcccatacgt taataattga tgcc 564

<210> 24
 <211> 188
 <212> PRT
 <213> Bacillus sp.

<400> 24
 Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Ala Val Leu
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Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe
 20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val
 35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu
 50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile
 65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu
85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu
100 105 110

Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys
115 120 125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu
130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg
145 150 155 160

Ser Asp Leu Trp Ala Lys Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg
165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Ile Asp Ala
180 185

<210> 25

<211> 2445

<212> DNA

<213> Bacillus sp.

<400> 25

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gcaggagat	atgatgctga	acaggcgact	acgacaggaa	atgccgtatt	cacgaccgag	180
cctgttgagg	acggcgagta	cgccggtcog	ggctacattt	ccttcttttc	tgaagattcc	240
tcgccacctt	cttcatcgac	aacctttcac	attcaggccg	ataaaacgga	gctctatcat	300
ttatctatcg	gatactatgc	tccatacggg	aacaagggaa	ccacaattct	ggtgaacggt	360
gcaggtaacg	gagagtttat	gttgccagcg	cccaggagcg	gggcagtcct	cgccgaagtg	420
gaaatttagca	aaatcctgct	cgaagaagga	aataatacga	ttacattcac	aagaggctgg	480
ggttattacg	gcattgaata	tattcgggtc	gagccgggta	atccaacggt	accgactata	540
tttattgaag	cagaagaaga	ttacgaagcg	actggaaatg	ttagcgttac	caatgaaatc	600
gaagggttatt	ccggagcagg	ctatgtgttc	aaccaagagg	ggacaattca	ttggaatgta	660
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aaacaaacaa	atctgacagt	gaatggacag	ggtagccgtca	atcttgactt	gaaagagaca	780
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caaaccgagt	tgaagacgc	caggtggatc	catgaacagg	tgggcaaata	tcctgcggtt	1080
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acccgtgcca	caacgtttga	tgtggagtac	gctttagaga	accgggaatc	tgaggatttc	1320
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caccataaac	taaacaattt	gatattggatg	tgggaattcgg	aagcggaaga	atggtatccg	1560
ggcgatgatg	tcgtggacat	gatcagtagc	gatatttata	atcctgtcgg	agatttcagt	1620
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cacctgcaaa	aggtgtttca	tcattgactac	gtcatcacc	tggatgaatt	gccggagaa	1860
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acgaggacga	cctccgaaat	tacagtgaac	tgggtcaaatg	ccattcaata	tgattccggt	1980
aatggctata	aattaattaa	agatggtgta	gagaccgttt	cagttgaagg	cggcgtgcaa	2040
gagtataacct	tcacaaattt	attgcccggg	acgcagtata	cgataaaagt	agaggcactg	2100
gaccaggatg	accgatggac	cgccgacgga	cgggtcgccg	ttgtatctac	attatccaac	2160
gctccgatata	cctatcctcc	ggctgatcact	cctgatgagc	cgaatgaaga	actgtccgag	2220
ggagagtata	cgctcttggc	agatgactta	tccagccagg	atggtgttct	ggaagtaagt	2280

cttgagccga cagttacgaa gctcattatt ccttctgcac tagccggcac attagacgga 2340
 gacttgagaa tcggttatgg ggacgtctgg atcgtcaccc cacacgaaca gcttgggggt 2400
 gacgagcagc aatccggcag cgcgtatgag ttagtgctgg agatc 2445

<210> 26
 <211> 815
 <212> PRT
 <213> Bacillus sp.

<400> 26
 Met Asn Lys Gln Pro Leu Lys Thr Ala Phe Ile Met Leu Leu Cys Ser
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 Val Phe Met Phe Gln Ser Leu Pro Tyr Tyr Val Asn Ala Ile Asn Glu
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 Gly Glu Arg Glu Ala Phe Ala Ser Ala Gly Arg Tyr Asp Ala Glu Gln
 35 40 45
 Ala Thr Thr Thr Gly Asn Ala Val Phe Thr Thr Glu Pro Val Glu Asp
 50 55 60
 Gly Glu Tyr Ala Gly Pro Gly Tyr Ile Ser Phe Phe Ser Glu Asp Ser
 65 70 75 80
 Ser Pro Pro Ser Ser Ser Thr Thr Phe His Ile Gln Ala Asp Lys Thr
 85 90 95
 Glu Leu Tyr His Leu Ser Ile Gly Tyr Tyr Ala Pro Tyr Gly Asn Lys
 100 105 110
 Gly Thr Thr Ile Leu Val Asn Gly Ala Gly Asn Gly Glu Phe Met Leu
 115 120 125
 Pro Ala Pro Glu Asp Gly Ala Val Ser Ala Glu Val Glu Ile Ser Lys
 130 135 140
 Ile Leu Leu Glu Glu Gly Asn Asn Thr Ile Thr Phe Thr Arg Gly Trp
 145 150 155 160
 Gly Tyr Tyr Gly Ile Glu Tyr Ile Arg Val Glu Pro Val Asn Pro Thr
 165 170 175
 Leu Pro Thr Ile Phe Ile Glu Ala Glu Glu Asp Tyr Glu Ala Thr Gly
 180 185 190
 Asn Val Ser Val Thr Asn Glu Ile Glu Gly Tyr Ser Gly Ala Gly Tyr
 195 200 205
 Leu Phe Asn Gln Glu Gly Thr Ile His Trp Asn Val Thr Ser Pro Glu
 210 215 220
 Thr Ser Ile Tyr Glu Val Ile Val Ala Tyr Ala Ala Pro Tyr Gly Asp
 225 230 235 240
 Lys Gln Thr Asn Leu Thr Val Asn Gly Gln Gly Thr Val Asn Leu Asp
 245 250 255
 Leu Lys Glu Thr Glu Val Phe Val Glu Leu Asn Val Gly Ile Val Ser
 260 265 270
 Leu Asn Glu Gly Glu Asn Thr Leu Thr Leu His Ser Gly Trp Gly Trp
 275 280 285
 Tyr Asn Ile Asp Tyr Ile Lys Leu Val Pro Val Val Ser Ser Asp Pro
 290 295 300

Glu Pro His Gln Val Glu Lys Thr Leu Val Asn Pro Asp Ala Ser Pro
 305 310 315 320
 Glu Ala Arg Ala Leu Ile Asn Tyr Leu Val Asp Gln Tyr Gly Asn Lys
 325 330 335
 Ile Leu Ser Gly Gln Thr Glu Leu Lys Asp Ala Arg Trp Ile His Glu
 340 345 350
 Gln Val Gly Lys Tyr Pro Ala Val Met Ala Val Asp Phe Met Asp Tyr
 355 360 365
 Ser Pro Ser Arg Val Val His Gly Ala Thr Gly Thr Ala Val Glu Glu
 370 375 380
 Ala Ile Glu Trp Ala Glu Met Gly Gly Ile Ile Thr Phe His Trp His
 385 390 395 400
 Trp Asn Ala Pro Lys Asp Leu Leu Asn Val Pro Gly Asn Glu Trp Trp
 405 410 415
 Ser Gly Phe Tyr Thr Arg Ala Thr Thr Phe Asp Val Glu Tyr Ala Leu
 420 425 430
 Glu Asn Arg Glu Ser Glu Asp Phe Gln Leu Leu Ile Ser Asp Met Asp
 435 440 445
 Val Ile Ala Glu Gln Leu Lys Arg Leu Gln Ala Glu Asn Ile Pro Val
 450 455 460
 Leu Trp Arg Pro Leu His Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly
 465 470 475 480
 Ala Lys Gly Pro Glu Ala Ala Ile Glu Leu Tyr Arg Leu Met Tyr Asp
 485 490 495
 Arg Tyr Thr Asn His His Lys Leu Asn Asn Leu Ile Trp Met Trp Asn
 500 505 510
 Ser Glu Ala Glu Glu Trp Tyr Pro Gly Asp Asp Val Val Asp Met Ile
 515 520 525
 Ser Thr Asp Ile Tyr Asn Pro Val Gly Asp Phe Ser Pro Ser Ile Asn
 530 535 540
 Lys Tyr Glu His Leu Lys Glu Leu Val Gln Asp Lys Lys Leu Val Ala
 545 550 555 560
 Leu Pro Glu Thr Gly Ile Ile Pro Asp Pro Asp Gln Leu Gln Leu Phe
 565 570 575
 Asn Ala Asn Trp Ser Trp Phe Ala Thr Trp Thr Gly Asp Tyr Ile Arg
 580 585 590
 Asp Gly Ile Ser Asn Pro Ile Glu His Leu Gln Lys Val Phe His His
 595 600 605
 Asp Tyr Val Ile Thr Leu Asp Glu Leu Pro Glu Asn Leu Ser Arg Tyr
 610 615 620
 Gly Leu Ser Glu Gly Val Trp Lys Ser Asp Ala Asp Leu Ser Val Lys
 625 630 635 640
 Thr Arg Thr Thr Ser Glu Ile Thr Val Asn Trp Ser Asn Ala Ile Gln
 645 650 655

Tyr Asp Ser Val Asn Gly Tyr Lys Leu Ile Lys Asp Gly Val Glu Thr
 660 665 670
 Val Ser Val Glu Gly Gly Val Gln Glu Tyr Thr Phe Thr Asn Leu Leu
 675 680 685
 Pro Gly Thr Gln Tyr Thr Ile Lys Val Glu Ala Leu Asp Gln Asp Asp
 690 695 700
 Arg Trp Thr Ala Asp Gly Pro Val Ala Val Val Ser Thr Leu Ser Asn
 705 710 715 720
 Ala Pro Ile Ser Tyr Pro Pro Ala Val Thr Pro Asp Glu Pro Asn Glu
 725 730 735
 Glu Leu Ser Glu Gly Glu Tyr Thr Leu Leu Ala Asp Asp Leu Ser Ser
 740 745 750
 Gln Asp Gly Val Leu Glu Val Ser Leu Glu Pro Thr Val Thr Lys Leu
 755 760 765
 Ile Ile Pro Ser Ala Leu Ala Gly Thr Leu Asp Gly Asp Leu Arg Ile
 770 775 780
 Gly Tyr Gly Asp Val Trp Ile Val Ile Pro His Glu Gln Leu Gly Gly
 785 790 795 800
 Asp Glu Gln Gln Ser Gly Ser Ala Tyr Glu Leu Val Leu Glu Ile
 805 810 815

<210> 27
 <211> 1488
 <212> DNA
 <213> Bacillus sp.

<400> 27
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 gtaagaatat ttgaagctga agatgctatt ttaaattgggc tgactattaa aaattctgaa 180
 ccagggtttt ctggtaccgg atatgtagggt gactttgaaa atagctctca gagtgtgacg 240
 tttcaaattg aggctcctaa agccggttta tacaacttaa atattggata tggcgcgatt 300
 tatggaagtg gaaaagtagc taatgttatt gtaaattggag agaagctaag tactttttaca 360
 atgggaagtg gcttttgtaa agcgctcagca ggaaagggtat tacttaattc aggccttaaat 420
 actatctcga ttactcctaa ttggacatgg tttaccattg attatatga agttatacat 480
 gcaccggaac cggaaaacca taatgtagaa aagacgttaa ttaaccctaa tgcaacggat 540
 gaagccaaag ctttaataag ctatctagtt gataactttg gtgagaaaat tcttgcaggg 600
 caacatgatt atccaaatac acgaccacga gatttagaat atatttatga aactactggg 660
 aagtatcctg ctgttttagg tttagacttt attgataaca gtccttctag agttgagcgc 720
 ggagcctctg ctgatgaaac accagtagct attgactggt ggaataaagg gggaatttgt 780
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 aagtcggagg actacatgct tctaatacgt gatattgatg taatagctgg tgaactaaag 960
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 gatagaatga cgaactacca taacttaaat aatttaatat gggtatggaa ttccattgaa 1140
 gaggattggt atcctggaga tgagtatgtc gatattgtaa gcttcgattc atatccagggt 1200
 gaatataact atagtccaat gagccgtgag tatgaagcac ttaaagagtt gtctagtaac 1260
 aagaaactta tagcaatagc agaaaatgga ccaataccag atcctgattt actacaactt 1320
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 agcgaagagc acctaagaaa agtatataat catgattatg tgattaccct aaataaatta 1440
 cctaacccta aaacatatag gggaagatgc acttatacag acactatc 1488



<400>	28															
Met	Arg	Asn	Glu	Lys	Ile	Arg	Pro	Phe	Thr	Lys	Ile	Lys	Ala	Ser	Val	
1				5					10					15		
Val	Thr	Ser	Val	Leu	Leu	Leu	Thr	Ile	Ser	Leu	Ile	Phe	Thr	Ile	Gly	
			20					25					30			
Asn	Ile	Ala	Asn	Ala	Glu	Ser	Glu	Val	Arg	Ile	Phe	Glu	Ala	Glu	Asp	
		35					40					45				
Ala	Ile	Leu	Asn	Gly	Leu	Thr	Ile	Lys	Asn	Ser	Glu	Pro	Gly	Phe	Ser	
	50					55					60					
Gly	Thr	Gly	Tyr	Val	Gly	Asp	Phe	Glu	Asn	Ser	Ser	Gln	Ser	Val	Thr	
65					70					75					80	
Phe	Gln	Ile	Glu	Ala	Pro	Lys	Ala	Gly	Leu	Tyr	Asn	Leu	Asn	Ile	Gly	
				85					90					95		
Tyr	Gly	Ala	Ile	Tyr	Gly	Ser	Gly	Lys	Val	Ala	Asn	Val	Ile	Val	Asn	
			100					105					110			
Gly	Glu	Lys	Leu	Ser	Thr	Phe	Thr	Met	Gly	Ser	Gly	Phe	Gly	Lys	Ala	
		115					120					125				
Ser	Ala	Gly	Lys	Val	Leu	Leu	Asn	Ser	Gly	Leu	Asn	Thr	Ile	Ser	Ile	
	130					135					140					
Thr	Pro	Asn	Trp	Thr	Trp	Phe	Thr	Ile	Asp	Tyr	Ile	Glu	Val	Ile	His	
145					150					155					160	
Ala	Pro	Glu	Pro	Glu	Asn	His	Asn	Val	Glu	Lys	Thr	Leu	Ile	Asn	Pro	
				165					170					175		
Asn	Ala	Thr	Asp	Glu	Ala	Lys	Ala	Leu	Ile	Ser	Tyr	Leu	Val	Asp	Asn	
			180					185					190			
Phe	Gly	Glu	Lys	Ile	Leu	Ala	Gly	Gln	His	Asp	Tyr	Pro	Asn	Thr	Arg	
		195					200					205				
Pro	Arg	Asp	Leu	Glu	Tyr	Ile	Tyr	Glu	Thr	Thr	Gly	Lys	Tyr	Pro	Ala	
	210					215					220					
Val	Leu	Gly	Leu	Asp	Phe	Ile	Asp	Asn	Ser	Pro	Ser	Arg	Val	Glu	Arg	
225					230					235					240	
Gly	Ala	Ser	Ala	Asp	Glu	Thr	Pro	Val	Ala	Ile	Asp	Trp	Trp	Asn	Lys	
				245					250					255		
Gly	Gly	Ile	Val	Thr	Phe	Thr	Trp	His	Trp	Asn	Ala	Pro	Lys	Asp	Leu	
			260					265					270			
Leu	Asp	Glu	Pro	Gly	Asn	Glu	Trp	Trp	Ser	Gly	Phe	Tyr	Thr	Arg	Ala	
		275					280					285				
Thr	Thr	Phe	Asp	Val	Glu	Tyr	Ala	Leu	Lys	His	Pro	Lys	Ser	Glu	Asp	
	290					295					300					
Tyr	Met	Leu	Leu	Ile	Arg	Asp	Ile	Asp	Val	Ile	Ala	Gly	Glu	Leu	Lys	
305					310					315					320	

Lys Leu Gln Glu Ala Asn Val Pro Val Leu Trp Arg Pro Leu His Glu
 325 330 335
 Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ser Thr
 340 345 350
 Lys Glu Leu Trp Arg Leu Met Tyr Asp Arg Met Thr Asn Tyr His Asn
 355 360 365
 Leu Asn Asn Leu Ile Trp Val Trp Asn Ser Ile Glu Glu Asp Trp Tyr
 370 375 380
 Pro Gly Asp Glu Tyr Val Asp Ile Val Ser Phe Asp Ser Tyr Pro Gly
 385 390 395 400
 Glu Tyr Asn Tyr Ser Pro Met Ser Arg Glu Tyr Glu Ala Leu Lys Glu
 405 410 415
 Leu Ser Ser Asn Lys Lys Leu Ile Ala Ile Ala Glu Asn Gly Pro Ile
 420 425 430
 Pro Asp Pro Asp Leu Leu Gln Leu Tyr His Ala Asn Tyr Ser Trp Phe
 435 440 445
 Ala Thr Trp Asn Gly Asp Ile Leu Arg Asn Gln Asn Ser Glu Glu His
 450 455 460
 Leu Arg Lys Val Tyr Asn His Asp Tyr Val Ile Thr Leu Asn Lys Leu
 465 470 475 480
 Pro Asn Leu Lys Thr Tyr Arg Gly Arg Cys Thr Tyr Thr Asp Thr Ile
 485 490 495

<210> 29
 <211> 1086
 <212> DNA
 <213> *Bacillus licheniformis*

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 gagctgatga attggcttgc tcatctgccg aaccgatcgg aaaatcgcgt actgtcaggt 180
 gcattcggcg gatattctaa tgcgacgttt tctatgaaag aagccaatcg aatcaaagat 240
 gctacagggc agtcacctgt cgtgtatgct tgtgattatt cgagaggatg gctggagaca 300
 gctcatattg ctgatgcgat cgattatagc tgtaacagcg atctaattct tcattggaag 360
 agcggaggca tacctcagat cagcatgcat ctctctaacc ctgctgttca atccggcaat 420
 tacaaaacaa agatctcaaa cagtcagtat gaaaaaatct tagactcatc aaccacagaa 480
 ggcaaacgat tggatgctgt actgagcaag gttgcagatg gccttcagca gttaaaaaat 540
 gaaggcgctt cagttctttt cagacctctt cacgaaatga acggagaatg gttctgggtg 600
 gggcttaccg gctataacca aaaggatagc gagcgaatat cactatacaa acagctttac 660
 caaaaaatct atcattatat gaccgataca agaggattgg acaacttgat ttgggtttat 720
 gcaccagacg ccaaccgcga ctttaagaca gacttttatt ctggggattc atatgttgat 780
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 ttagcttggg atgaggttg gagccctgcg gctaatacagg gtgcctttta tctctataat 1020
 gacagttgga cgctgaataa gggagagcta tgggaaggca gctcacttac accggcagcc 1080
 gaataa 1086

<210> 30
 <211> 361
 <212> PRT
 <213> Bacillus licheniformis

<400> 30
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 Ser Ala Phe Ser Gln Thr Ala Ser Ala His Thr Val Asn Pro Val Asn
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 Gln Asn Ala Gln Ser Thr Thr Lys Glu Leu Met Asn Trp Leu Ala His
 35 40 45
 Leu Pro Asn Arg Ser Glu Asn Arg Val Leu Ser Gly Ala Phe Gly Gly
 50 55 60
 Tyr Ser Asn Ala Thr Phe Ser Met Lys Glu Ala Asn Arg Ile Lys Asp
 65 70 75 80
 Ala Thr Gly Gln Ser Pro Val Val Tyr Ala Cys Asp Tyr Ser Arg Gly
 85 90 95
 Trp Leu Glu Thr Ala His Ile Ala Asp Ala Ile Asp Tyr Ser Cys Asn
 100 105 110
 Ser Asp Leu Ile Ser His Trp Lys Ser Gly Gly Ile Pro Gln Ile Ser
 115 120 125
 Met His Leu Pro Asn Pro Ala Phe Gln Ser Gly Asn Tyr Lys Thr Lys
 130 135 140
 Ile Ser Asn Ser Gln Tyr Glu Lys Ile Leu Asp Ser Ser Thr Thr Glu
 145 150 155 160
 Gly Lys Arg Leu Asp Ala Val Leu Ser Lys Val Ala Asp Gly Leu Gln
 165 170 175
 Gln Leu Lys Asn Glu Gly Val Pro Val Leu Phe Arg Pro Leu His Glu
 180 185 190
 Met Asn Gly Glu Trp Phe Trp Trp Gly Leu Thr Gly Tyr Asn Gln Lys
 195 200 205
 Asp Ser Glu Arg Ile Ser Leu Tyr Lys Gln Leu Tyr Gln Lys Ile Tyr
 210 215 220
 His Tyr Met Thr Asp Thr Arg Gly Leu Asp Asn Leu Ile Trp Val Tyr
 225 230 235 240
 Ala Pro Asp Ala Asn Arg Asp Phe Lys Thr Asp Phe Tyr Pro Gly Asp
 245 250 255
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